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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/848,164

DATE: 06/26/2001
TIME: 15:15:09

Input Set : N:\Crf3\RULE60\09848164.txt
Output Set: N:\CRF3\06262001\I848164.raw

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ENTERED

SEQUENCE LISTING

4 (1) GENERAL INFORMATION:
 6 (i) APPLICANT: Rhode, Peter R.
 7 Jiao, Jin-An
 8 Burkhardt, Martin
 9 Wong, Hing
 11 (ii) TITLE OF INVENTION: MHC COMPLEXES AND USES THEREOF
 13 (iii) NUMBER OF SEQUENCES: 124
 15 (iv) CORRESPONDENCE ADDRESS:
 16 (A) ADDRESSEE: Dade International, Inc.
 17 (B) STREET: 1717 Deerfield Road
 18 (C) CITY: Deerfield
 19 (D) STATE: Illinois
 20 (E) COUNTRY: USA
 21 (F) ZIP: 60015
 23 (v) COMPUTER READABLE FORM:
 24 (A) MEDIUM TYPE: Floppy disk
 25 (B) COMPUTER: IBM PC compatible
 26 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 27 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
 29 (vi) CURRENT APPLICATION DATA:
 C--> 30 (A) APPLICATION NUMBER: US/09/848,164
 C--> 31 (B) FILING DATE: 03-May-2001
 32 (C) CLASSIFICATION:
 42 (vii) PRIOR APPLICATION DATA:
 35 (A) APPLICATION NUMBER: 09/067,615
 36 (B) FILING DATE:
 39 (A) APPLICATION NUMBER: US 08/382,454
 40 (B) FILING DATE: 01-FEB-1995
 43 (A) APPLICATION NUMBER: US 08/283,302
 44 (B) FILING DATE: 29-JUL-1994
 46 (viii) ATTORNEY/AGENT INFORMATION:
 47 (A) NAME: Pearson, Louise S.
 48 (B) REGISTRATION NUMBER: 32,369
 49 (C) REFERENCE/DOCKET NUMBER: STR-4665-CIP2
 51 (ix) TELECOMMUNICATION INFORMATION:
 52 (A) TELEPHONE: (708) 267-5300
 53 (B) TELEFAX: (708) 267-5376
 56 (2) INFORMATION FOR SEQ ID NO: 1:
 58 (i) SEQUENCE CHARACTERISTICS:
 59 (A) LENGTH: 10 amino acids
 60 (B) TYPE: amino acid
 61 (C) STRANDEDNESS: unknown
 62 (D) TOPOLOGY: unknown
 64 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
 66 Ala Ser Gly Gly Gly Ser Gly Gly Gly
 67 1 5 10

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70 (2) INFORMATION FOR SEQ ID NO: 2:
72 (i) SEQUENCE CHARACTERISTICS:
73 (A) LENGTH: 8 base pairs
74 (B) TYPE: nucleic acid
75 (C) STRANDEDNESS: unknown
76 (D) TOPOLOGY: unknown
78 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
80 CCACCATG 8
83 (2) INFORMATION FOR SEQ ID NO: 3:
85 (i) SEQUENCE CHARACTERISTICS:
86 (A) LENGTH: 18 amino acids
87 (B) TYPE: amino acid
88 (C) STRANDEDNESS: unknown
89 (D) TOPOLOGY: unknown
91 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
93 Ser Ile Ser Gln Ala Val His Ala Ala His Ala Glu Ile Asn Glu Ala
94 1 5 10 15
96 Gly Arg
99 (2) INFORMATION FOR SEQ ID NO: 4:
101 (i) SEQUENCE CHARACTERISTICS:
102 (A) LENGTH: 18 amino acids
103 (B) TYPE: amino acid
104 (C) STRANDEDNESS: unknown
105 (D) TOPOLOGY: unknown
107 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
110 Ser Ile Ser Gln Ala Val His Ala Ala Arg Ala Glu Ile Asn Glu Ala
111 1 5 10 15
113 Gly Arg
116 (2) INFORMATION FOR SEQ ID NO: 5:
118 (i) SEQUENCE CHARACTERISTICS:
119 (A) LENGTH: 18 amino acids
120 (B) TYPE: amino acid
121 (C) STRANDEDNESS: unknown
122 (D) TOPOLOGY: unknown
124 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
126 Ser Ile Ser Gln Ala Val His Ala Ala His Tyr Glu Ile Asn Glu Ala
127 1 5 10 15
129 Gly Arg
132 (2) INFORMATION FOR SEQ ID NO: 6:
134 (i) SEQUENCE CHARACTERISTICS:
135 (A) LENGTH: 13 amino acids
136 (B) TYPE: amino acid
137 (C) STRANDEDNESS: unknown
138 (D) TOPOLOGY: unknown
140 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
142 Asn Leu Cys Asn Ile Pro Cys Ser Ala Leu Leu Ser Ser
143 1 5 10
146 (2) INFORMATION FOR SEQ ID NO: 7:
148 (i) SEQUENCE CHARACTERISTICS:

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149 (A) LENGTH: 11 amino acids
150 (B) TYPE: amino acid
151 (C) STRANDEDNESS: unknown
152 (D) TOPOLOGY: unknown
154 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
156 Gln Ile Ser Val Gln Pro Ala Phe Ser Val Gln
157 1 5 10
160 (2) INFORMATION FOR SEQ ID NO: 8:
162 (i) SEQUENCE CHARACTERISTICS:
163 (A) LENGTH: 13 amino acids
164 (B) TYPE: amino acid
165 (C) STRANDEDNESS: unknown
166 (D) TOPOLOGY: unknown
168 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:
170 Pro Lys Tyr Val Lys Gln Asn Thr Leu Lys Leu Ala Thr
171 1 5 10
174 (2) INFORMATION FOR SEQ ID NO: 9:
176 (i) SEQUENCE CHARACTERISTICS:
177 (A) LENGTH: 13 amino acids
178 (B) TYPE: amino acid
179 (C) STRANDEDNESS: unknown
180 (D) TOPOLOGY: unknown
182 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:
184 His Tyr Gly Ser Leu Pro Gln Lys Ser Gln His Gly Arg
185 1 5 10
188 (2) INFORMATION FOR SEQ ID NO: 10:
190 (i) SEQUENCE CHARACTERISTICS:
191 (A) LENGTH: 13 amino acids
192 (B) TYPE: amino acid
193 (C) STRANDEDNESS: unknown
194 (D) TOPOLOGY: unknown
196 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:
198 His Ser Leu Gly Lys Trp Leu Gly His Pro Asp Lys Phe
199 1 5 10
202 (2) INFORMATION FOR SEQ ID NO: 11:
204 (i) SEQUENCE CHARACTERISTICS:
205 (A) LENGTH: 14 amino acids
206 (B) TYPE: amino acid
207 (C) STRANDEDNESS: unknown
208 (D) TOPOLOGY: unknown
210 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:
212 Met Ala Ser Gln Lys Arg Pro Ser Gln Arg Ser Lys Tyr Leu
213 1 5 10
216 (2) INFORMATION FOR SEQ ID NO: 12:
218 (i) SEQUENCE CHARACTERISTICS:
219 (A) LENGTH: 27 base pairs
220 (B) TYPE: nucleic acid
221 (C) STRANDEDNESS: unknown
222 (D) TOPOLOGY: unknown

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224	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:	
226	GCAGAAGAAT TCGAGCTCGG CCCCCAG	27
229	(2) INFORMATION FOR SEQ ID NO: 13:	
231	(i) SEQUENCE CHARACTERISTICS:	
232	(A) LENGTH: 33 base pairs	
233	(B) TYPE: nucleic acid	
234	(C) STRANDEDNESS: unknown	
235	(D) TOPOLOGY: unknown	
237	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:	
239	GATGATATCA GAGAGAAATA CATACTAACAC	33
242	(2) INFORMATION FOR SEQ ID NO: 14:	
244	(i) SEQUENCE CHARACTERISTICS:	
245	(A) LENGTH: 30 base pairs	
246	(B) TYPE: nucleic acid	
247	(C) STRANDEDNESS: unknown	
248	(D) TOPOLOGY: unknown	
250	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:	
252	CGGAAGAAAG AGACTTCGGC CGCTACTTAC	30
255	(2) INFORMATION FOR SEQ ID NO: 15:	
257	(i) SEQUENCE CHARACTERISTICS:	
258	(A) LENGTH: 47 base pairs	
259	(B) TYPE: nucleic acid	
260	(C) STRANDEDNESS: unknown	
261	(D) TOPOLOGY: unknown	
263	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:	
265	GTGTGTTAGT ATGTATTCT CTCTGATATC TTCAGCTTCC AGCAGTG	47
268	(2) INFORMATION FOR SEQ ID NO: 16:	
270	(i) SEQUENCE CHARACTERISTICS:	
271	(A) LENGTH: 21 base pairs	
272	(B) TYPE: nucleic acid	
273	(C) STRANDEDNESS: unknown	
274	(D) TOPOLOGY: unknown	
276	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:	
278	TCTTCTAGAA GACCACGCTA C	21
281	(2) INFORMATION FOR SEQ ID NO: 17:	
283	(i) SEQUENCE CHARACTERISTICS:	
284	(A) LENGTH: 36 base pairs	
285	(B) TYPE: nucleic acid	
286	(C) STRANDEDNESS: unknown	
287	(D) TOPOLOGY: unknown	
289	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:	
291	GATGATATCC GGCGGAAGTC TCTTCTTCC GTTGTC	36
294	(2) INFORMATION FOR SEQ ID NO: 18:	
296	(i) SEQUENCE CHARACTERISTICS:	
297	(A) LENGTH: 24 base pairs	
298	(B) TYPE: nucleic acid	
299	(C) STRANDEDNESS: unknown	
300	(D) TOPOLOGY: unknown	
302	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:	

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304 CAGGGTTATC AACACCCTGA AAAC 24
 306 (2) INFORMATION FOR SEQ ID NO: 19:
 308 (i) SEQUENCE CHARACTERISTICS:
 309 (A) LENGTH: 21 base pairs
 310 (B) TYPE: nucleic acid
 311 (C) STRANDEDNESS: unknown
 312 (D) TOPOLOGY: unknown
 314 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:
 316 GTCACAGTTA TCCACTCTGT C 21
 319 (2) INFORMATION FOR SEQ ID NO: 20:
 321 (i) SEQUENCE CHARACTERISTICS:
 322 (A) LENGTH: 38 base pairs
 323 (B) TYPE: nucleic acid
 324 (C) STRANDEDNESS: unknown
 325 (D) TOPOLOGY: unknown
 327 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:
 329 CCGTCTCCTC AGGTACGGCC GGCCTCTCCA GGTCTTCG 38
 332 (2) INFORMATION FOR SEQ ID NO: 21:
 334 (i) SEQUENCE CHARACTERISTICS:
 335 (A) LENGTH: 39 base pairs
 336 (B) TYPE: nucleic acid
 337 (C) STRANDEDNESS: unknown
 338 (D) TOPOLOGY: unknown
 340 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:
 342 CACAGTTATC CACTCTGTCT TTGATATCAC AGGTGTCT 39
 345 (2) INFORMATION FOR SEQ ID NO: 22:
 347 (i) SEQUENCE CHARACTERISTICS:
 348 (A) LENGTH: 13 amino acids
 349 (B) TYPE: amino acid
 350 (C) STRANDEDNESS: unknown
 351 (D) TOPOLOGY: unknown
 353 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:
 355 His Ser Leu Gly Lys Tyr Leu Gly His Pro Asp Lys Phe
 356 1 5 10
 359 (2) INFORMATION FOR SEQ ID NO: 23:
 361 (i) SEQUENCE CHARACTERISTICS:
 362 (A) LENGTH: 13 amino acids
 363 (B) TYPE: amino acid
 364 (C) STRANDEDNESS: unknown
 365 (D) TOPOLOGY: unknown
 367 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:
 369 His Ser Leu Gly Lys Leu Leu Gly His Pro Asp Lys Phe
 370 1 5 10
 373 (2) INFORMATION FOR SEQ ID NO: 24:
 375 (i) SEQUENCE CHARACTERISTICS:
 376 (A) LENGTH: 18 amino acids
 377 (B) TYPE: amino acid
 378 (C) STRANDEDNESS: unknown
 379 (D) TOPOLOGY: unknown

VERIFICATION SUMMARY
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Input Set : N:\Crf3\RULE60\09848164.txt
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L:30 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:31 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:1861 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:122
L:1865 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:122
L:1869 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:122
L:1873 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:122
L:1877 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:122
L:1881 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:122
L:1885 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:122
L:1889 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:122
L:1893 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:122
L:1897 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:122
L:1901 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:122
L:1905 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:122
L:1909 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:122
L:1913 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:122
L:1917 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:122
L:1921 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:122
L:1925 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:122
L:1929 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:122
L:1933 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:122
L:1937 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:122
L:1941 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:122
L:1945 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:122
L:1949 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:122
L:1953 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:122
L:1957 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:122
L:1961 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:122
L:1965 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:122
L:1969 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:122
L:1973 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:122
L:1977 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:122
L:1981 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:122
L:1985 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:122
L:2006 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:123
L:2010 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:123
L:2014 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:123
L:2018 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:123
L:2022 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:123
L:2026 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:123
L:2030 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:123
L:2034 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:123
L:2038 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:123
L:2042 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:123
L:2046 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:123
L:2050 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:123
L:2054 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:123
L:2058 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:123

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Input Set : N:\Crf3\RULE60\09848164.txt
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L:2062 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:123
L:2066 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:123
L:2070 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:123
L:2074 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:123